



SEQUENCE LISTING

<110> Oppmann, Birgit
De Waal Malefyt, Rene
Rennick, Donna M.
Kastelein, Robert A.
Wiekowski, Maria T.
Lira, Sergio A.
Narula, Satwant K.

<120> Mammalian Genes; Related Reagents and
Methods

<130> 16622-005001/ DX01042X

<140> US 09/658,699
<141> 2000-09-08

<150> US 60/164,616
<151> 1999-11-10

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<151> 1999-09-09

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<220>
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Ala Gln Gly Arg Ala Val Pro Gly Gly Ser Ser Pro Ala Trp Thr Gln
-5 -1 1 5 10

tgc cag cag ctt tca cag aag ctc tgc aca ctg gcc tgg agt gca cat 144

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cca	cta	gtg	gga	cac	atg	gat	cta	aga	gaa	gag	gga	gat	gaa	gag	act	192
Pro	Leu	Val	Gly	His	Met	Asp	Leu	Arg	Glu	Glu	Gly	Asp	Glu	Glu	Thr	
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Thr	Asn	Asp	Val	Pro	His	Ile	Gln	Cys	Gly	Asp	Gly	Cys	Asp	Pro	Gln	
45							50					55				
gga	ctc	agg	gac	aac	agt	cag	ttc	tgc	ttg	caa	agg	atc	cac	cag	ggt	288
Gly	Leu	Arg	Asp	Asn	Ser	Gln	Phe	Cys	Leu	Gln	Arg	Ile	His	Gln	Gly	
60							65					70		75		
ctg	att	ttt	tat	gag	aag	ctg	cta	gga	tcg	gat	att	ttc	aca	ggg	gag	336
Leu	Ile	Phe	Tyr	Glu	Lys	Leu	Leu	Gly	Ser	Asp	Ile	Phe	Thr	Gly	Glu	
80							85					90				
cct	tct	ctg	ctc	cct	gat	agc	cct	gtg	gcg	cag	ctt	cat	gcc	tcc	cta	384
Pro	Ser	Leu	Leu	Pro	Asp	Ser	Pro	Val	Ala	Gln	Leu	His	Ala	Ser	Leu	
95							100					105				
ctg	ggc	ctc	agc	caa	ctc	cag	cct	gag	ggt	cac	cac	tgg	gag	act	432	
Leu	Gly	Leu	Ser	Gln	Leu	Leu	Gln	Pro	Glu	Gly	His	His	Trp	Glu	Thr	
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Gln	Gln	Ile	Pro	Ser	Leu	Ser	Pro	Ser	Gln	Pro	Trp	Gln	Arg	Leu	Leu	
125							130					135				
ctc	cgc	ttc	aaa	atc	ctt	cgc	agc	ctc	cag	gcc	ttt	gtg	gct	gta	gcc	528
Leu	Arg	Phe	Lys	Ile	Leu	Arg	Ser	Leu	Gln	Ala	Phe	Val	Ala	Val	Ala	
140							145					150		155		
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Cys Gln Gln Leu Ser Gln Lys Leu Cys Thr Leu Ala Trp Ser Ala His																
15 20 25																

Pro	Leu	Val	Gly	His	Met	Asp	Leu	Arg	Glu	Glu	Gly	Asp	Glu	Glu	Thr
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Thr	Asn	Asp	Val	Pro	His	Ile	Gln	Cys	Gly	Asp	Gly	Cys	Asp	Pro	Gln
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Leu	Ile	Phe	Tyr	Glu	Lys	Leu	Leu	Gly	Ser	Asp	Ile	Phe	Thr	Gly	Glu
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Pro	Ser	Leu	Leu	Pro	Asp	Ser	Pro	Val	Ala	Gln	Leu	His	Ala	Ser	Leu
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Leu	Gly	Leu	Ser	Gln	Leu	Leu	Gln	Pro	Glu	Gly	His	His	Trp	Glu	Thr
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Leu	Arg	Phe	Lys	Ile	Leu	Arg	Ser	Leu	Gln	Ala	Phe	Val	Ala	Val	Ala
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Ala	Arg	Val	Phe	Ala	His	Gly	Ala	Ala	Thr	Leu	Ser	Pro			
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<213> Unknown Organism

<220>
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<222> (113) . . (700)

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<222> (176)..(700)
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Met Leu
-20

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gat tgc aga gca gta ata atg cta tgg ctg ttg ccc tgg gtc act cag      166
Asp Cys Arg Ala Val Ile Met Leu Trp Leu Leu Pro Trp Val Thr Gln
-15          -10          -5

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ggc ctg gct gtg cct agg agt agc agt cct gac tgg qct caq tqc caq 214

Gly	Leu	Ala	Val	Pro	Arg	Ser	Ser	Ser	Pro	Asp	Trp	Ala	Gln	Cys	Gln			
-1	1					5						10						
cag	ctc	tct	cg	aat	ctc	tgc	atg	cta	gcc	tgg	aac	gca	cat	gca	cca	262		
Gln	Leu	Ser	Arg	Asn	Leu	Cys	Met	Leu	Ala	Trp	Asn	Ala	His	Ala	Pro			
15					20						25							
g	cg	g	g	cat	atg	aat	cta	cta	aga	gaa	gaa	gag	gat	gaa	gag	act	aaa	310
Ala	Gly	His	Met	Asn	Leu	Leu	Arg	Glu	Glu	Glu	Asp	Glu	Glu	Thr	Lys			
30					35						40			45				
aat	aat	gtg	ccc	cgt	atc	cag	tgt	gaa	gat	ggt	tgt	gac	cca	caa	gga		358	
Asn	Asn	Val	Pro	Arg	Ile	Gln	Cys	Glu	Asp	Gly	Cys	Asp	Pro	Gln	Gly			
50					55						60							
ctc	aag	gac	aac	agc	cag	ttc	tgc	ttg	caa	agg	atc	cgc	caa	ggt	ctg		406	
Leu	Lys	Asp	Asn	Ser	Gln	Phe	Cys	Leu	Gln	Arg	Ile	Arg	Gln	Gly	Leu			
65					70						75							
gct	ttt	tat	aag	cac	ctg	ctt	gac	tac	atc	ttc	aaa	ggg	gag	cct		454		
Ala	Phe	Tyr	Lys	His	Leu	Leu	Asp	Ser	Asp	Ile	Phe	Lys	Gly	Glu	Pro			
80					85						90							
gct	cta	ctc	cct	gat	agc	ccc	atg	gag	caa	ctt	cac	acc	tcc	cta	cta		502	
Ala	Leu	Leu	Pro	Asp	Ser	Pro	Met	Glu	Gln	Leu	His	Thr	Ser	Leu	Leu			
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Gln	Met	Pro	Ser	Leu	Ser	Ser	Gln	Gln	Gln	Trp	Gln	Arg	Pro	Leu	Leu			
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cgt	tcc	aag	atc	ctt	cga	agc	ctc	cag	gcc	ttt	ttg	gcc	ata	gct	gcc		646	
Arg	Ser	Lys	Ile	Leu	Arg	Ser	Leu	Gln	Ala	Phe	Leu	Ala	Ile	Ala	Ala			
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Arg	Val	Phe	Ala	His	Gly	Ala	Ala	Thr	Leu	Thr	Glu	Pro	Leu	Val	Pro			
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Thr	Ala																	
175																		
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aaaggggaac attatactt cctgggtggc tcagggaaat gtgcagatgc acagtactcc 1110
agacagcagc tctgtacctg cctgctctgt ccctcagttc taacagaatc tagtcactaa 1170
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<211> 196
<212> PRT
<213> Unknown Organism

<220>
<223> surmised Mus sp.

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-5 -1 1 5 10

Cys Gln Gln Leu Ser Arg Asn Leu Cys Met Leu Ala Trp Asn Ala His
15 20 25

Ala Pro Ala Gly His Met Asn Leu Leu Arg Glu Glu Glu Asp Glu Glu
30 35 40

Thr Lys Asn Asn Val Pro Arg Ile Gln Cys Glu Asp Gly Cys Asp Pro
45 50 55

Gln Gly Leu Lys Asp Asn Ser Gln Phe Cys Leu Gln Arg Ile Arg Gln
60 65 70 75

Gly Leu Ala Phe Tyr Lys His Leu Leu Asp Ser Asp Ile Phe Lys Gly
80 85 90

Glu Pro Ala Leu Leu Pro Asp Ser Pro Met Glu Gln Leu His Thr Ser
95 100 105

Leu Leu Gly Leu Ser Gln Leu Leu Gln Pro Glu Asp His Pro Arg Glu
110 115 120

Thr Gln Gln Met Pro Ser Leu Ser Ser Ser Gln Gln Trp Gln Arg Pro
125 130 135

Leu Leu Arg Ser Lys Ile Leu Arg Ser Leu Gln Ala Phe Leu Ala Ile
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Ala Ala Arg Val Phe Ala His Gly Ala Ala Thr Leu Thr Glu Pro Leu
160 165 170

Val Pro Thr Ala
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<210> 5

<211> 102
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 <213> Unknown Organism

<220>
 <223> Description of Unknown Organism: surmised Sus sp.

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Leu Gly Ser Asp Ile Phe Thr Gly Glu Pro Ser Leu His Pro Asp Gly
 20 25 30

Ser Val Gly Gln Leu His Ala Ser Leu Leu Gly Leu Arg Gln Leu Leu
 35 40 45

Gln Pro Glu Gly His His Trp Glu Thr Glu Gln Thr Pro Ser Pro Ser
 50 55 60

Pro Ser Gln Pro Trp Gln Arg Leu Leu Leu Arg Leu Lys Ile Leu Arg
 65 70 75 80

Ser Leu Gln Ala Phe Val Ala Val Ala Arg Val Phe Ala His Gly
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Ala Ala Thr Leu Ser Gln
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<210> 6
 <211> 306
 <212> PRT
 <213> Homo sapiens

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Glu Asp Gly Ile Thr Trp Thr Leu Asp Gln Ser Ser Glu Val Leu Gly
 35 40 45

Ser Gly Lys Thr Leu Thr Ile Gln Val Lys Glu Phe Gly Asp Ala Gly
 50 55 60

Gln Tyr Thr Cys His Lys Gly Gly Glu Val Leu Ser His Ser Leu Leu
 65 70 75 80

Leu Leu His Lys Lys Glu Asp Gly Ile Trp Ser Thr Asp Ile Leu Lys
 85 90 95

Asp Gln Lys Glu Pro Lys Asn Lys Thr Phe Leu Arg Cys Glu Ala Lys
 100 105 110

Asn Tyr Ser Gly Arg Phe Thr Cys Trp Trp Leu Thr Thr Ile Ser Thr
 115 120 125

Asp Leu Thr Phe Ser Val Lys Ser Ser Arg Gly Ser Ser Asp Pro Gln
 130 135 140

Gly Val Thr Cys Gly Ala Ala Thr Leu Ser Ala Glu Arg Val Arg Gly
 145 150 155 160

Asp Asn Lys Glu Tyr Glu Tyr Ser Val Glu Cys Gln Glu Asp Ser Ala

	165		170		175
Cys Pro Ala Ala Glu Glu Ser Leu Pro Ile Glu Val Met Val Asp Ala					
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Val His Lys Leu Lys Tyr Glu Asn Tyr Thr Ser Ser Phe Phe Ile Arg					
195		200		205	
Asp Ile Ile Lys Pro Asp Pro Pro Lys Asn Leu Gln Leu Lys Pro Leu					
210		215		220	
Lys Asn Ser Arg Gln Val Glu Val Ser Trp Glu Tyr Pro Asp Thr Trp					
225		230		235	
Ser Thr Pro His Ser Tyr Phe Ser Leu Thr Phe Cys Val Gln Val Gln					
245		250		255	
Gly Lys Ser Lys Arg Glu Lys Lys Asp Arg Val Phe Thr Asp Lys Thr					
260		265		270	
Ser Ala Thr Val Ile Cys Arg Lys Asn Ala Ser Ile Ser Val Arg Ala					
275		280		285	
Gln Asp Arg Tyr Tyr Ser Ser Ser Trp Ser Glu Trp Ala Ser Val Pro					
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Cys Ser					
305					

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<212> DNA
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cgtttatgtt gtagagggtgg actggactcc cgatgcccct ggagaaaacag tgaacctcac
ctgtgacacg cctgaagaag atgacatcac ctggaccta gaccagagac atggagtcat
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ctgcccacaaa ggaggcgaga ctctgagcca ctcacatctg ctgctccaca agaaggaaaa
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ccagaaaggt gcgttcctcg tagagaagac atctaccgaa gtccaatgca aaggcgggaa
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aagttgactc tgaagagttt agcactagtt tcaacaccaa gaaagacttt ttagaagtga
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<211> 335
<212> PRT
<213> Mus musculus

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35 40 45
Thr Cys Asp Thr Pro Glu Glu Asp Asp Ile Thr Trp Thr Ser Asp Gln
50 55 60
Arg His Gly Val Ile Gly Ser Gly Lys Thr Leu Thr Ile Thr Val Lys
65 70 75 80
Glu Phe Leu Asp Ala Gly Gln Tyr Thr Cys His Lys Gly Gly Glu Thr
85 90 95
Leu Ser His Ser His Leu Leu His Lys Lys Glu Asn Gly Ile Trp
100 105 110
Ser Thr Glu Ile Leu Lys Asn Phe Lys Asn Lys Thr Phe Leu Lys Cys
115 120 125
Glu Ala Pro Asn Tyr Ser Gly Arg Phe Thr Cys Ser Trp Leu Val Gln
130 135 140
Arg Asn Met Asp Leu Lys Phe Asn Ile Lys Ser Ser Ser Ser Ser Pro
145 150 155 160
Asp Ser Arg Ala Val Thr Cys Gly Met Ala Ser Leu Ser Ala Glu Lys
165 170 175
Val Thr Leu Asp Gln Arg Asp Tyr Glu Lys Tyr Ser Val Ser Cys Gln
180 185 190
Glu Asp Val Thr Cys Pro Thr Ala Glu Glu Thr Leu Pro Ile Glu Leu
195 200 205
Ala Leu Glu Ala Arg Gln Gln Asn Lys Tyr Glu Asn Tyr Ser Thr Ser
210 215 220
Phe Phe Ile Arg Asp Ile Ile Lys Pro Asp Pro Pro Lys Asn Leu Gln
225 230 235 240
Met Lys Pro Leu Lys Asn Ser Gln Val Glu Val Ser Trp Glu Tyr Pro
245 250 255
Asp Ser Trp Ser Thr Pro His Ser Tyr Phe Ser Leu Lys Phe Phe Val
260 265 270
Arg Ile Gln Arg Lys Lys Glu Lys Met Lys Glu Thr Glu Glu Gly Cys
275 280 285
Asn Gln Lys Gly Ala Phe Leu Val Glu Lys Thr Ser Thr Glu Val Gln
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Cys Lys Gly Gly Asn Val Cys Val Gln Ala Gln Asp Arg Tyr Tyr Asn
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Ser Ser Cys Ser Lys Trp Ala Cys Val Pro Cys Arg Val Arg Ser
325 330 335

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<211> 1008
<212> DNA
<213> Rattus norvegicus

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acctcagacc	agagacgtgg	agtcatagc	tctggaaaga	ccctgaccat	cactgtcaga	240
gagtttctag	atgctggcca	atacacctgc	cacagaggag	gcgagactct	gagccactca	300
catctgctgc	tccacaagaa	ggaaaatgga	atttggtcca	ccgagatttt	aaaaaatttc	360
aaaaataaga	ctttcctgaa	gtgtgaagca	ccaaactact	ccggacgggtt	cacctgctca	420
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gagtctcggg	cggtgacatg	tggacgagca	tctctgtctg	cagagaaggt	cacactgaac	540
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gaggagaccc	tgcccattga	actgggtggt	gaggcccagc	agcagaataa	atatgagaac	660
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gccgaagtcc	aatgcaaagg	ggcgaatatac	tgcgtgcag	cgcaggaccg	ctactacaat	960
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<210> 10

<211> 335

<212> PRT

<213> Rattus norvegicus

<400> 10

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						20			25				30		
Val	Glu	Val	Asp	Trp	Arg	Pro	Asp	Ala	Pro	Gly	Glu	Thr	Val	Thr	Leu
						35			40			45			
Thr	Cys	Asp	Ser	Pro	Glu	Glu	Asp	Asp	Ile	Thr	Trp	Thr	Ser	Asp	Gln
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Arg	Arg	Gly	Val	Ile	Gly	Ser	Gly	Lys	Thr	Leu	Thr	Ile	Thr	Val	Arg
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Glu	Phe	Leu	Asp	Ala	Gly	Gln	Tyr	Thr	Cys	His	Arg	Gly	Gly	Glu	Thr
						85			90			95			
Leu	Ser	His	Ser	His	Leu	Leu	Leu	His	Lys	Lys	Glu	Asn	Gly	Ile	Trp
						100			105			110			
Ser	Thr	Glu	Ile	Leu	Lys	Asn	Phe	Lys	Asn	Lys	Thr	Phe	Leu	Lys	Cys
						115			120			125			
Glu	Ala	Pro	Asn	Tyr	Ser	Gly	Arg	Phe	Thr	Cys	Ser	Trp	Leu	Val	His
						130			135			140			
Arg	Asn	Thr	Asp	Leu	Lys	Phe	Asn	Ile	Lys	Ser	Ser	Ser	Ser	Ser	Pro
						145			150			155			160
Glu	Ser	Arg	Ala	Val	Thr	Cys	Gly	Arg	Ala	Ser	Leu	Ser	Ala	Glu	Lys
						165			170			175			
Val	Thr	Leu	Asn	Gln	Arg	Asp	Tyr	Glu	Lys	Tyr	Ser	Val	Ala	Cys	Gln
						180			185			190			
Glu	Asp	Val	Thr	Cys	Pro	Thr	Ala	Glu	Glu	Thr	Leu	Pro	Ile	Glu	Leu
						195			200			205			
Val	Val	Glu	Ala	Gln	Gln	Gln	Asn	Lys	Tyr	Glu	Asn	Tyr	Ser	Thr	Ser
						210			215			220			
Phe	Phe	Ile	Arg	Asp	Ile	Ile	Lys	Pro	Asp	Pro	Pro	Lys	Asn	Leu	Gln
							225			230			235		240
Val	Lys	Pro	Leu	Lys	Asn	Ser	Gln	Val	Glu	Val	Ser	Trp	Glu	Tyr	Pro
							245			250			255		
Asp	Ser	Trp	Ser	Thr	Pro	His	Ser	Tyr	Phe	Ser	Leu	Lys	Phe	Phe	Val
							260			265			270		

Arg	Ile	Gln	Arg	Lys	Lys	Glu	Lys	Thr	Lys	Glu	Thr	Glu	Glu	Glu	Cys
275						280					285				
Asn	Gln	Lys	Gly	Ala	Phe	Leu	Val	Glu	Lys	Thr	Ser	Ala	Glu	Val	Gln
290						295					300				
Cys	Lys	Gly	Ala	Asn	Ile	Cys	Val	Gln	Ala	Gln	Asp	Arg	Tyr	Tyr	Asn
305						310				315				320	
Ser	Ser	Cys	Ser	Lys	Trp	Thr	Cys	Val	Pro	Cys	Arg	Gly	Arg	Ser	
						325			330				335		

<210> 11
<211> 821
<212> DNA
<213> Rattus norvegicus

<400> 11

ctcgacgcag	agcaagatgt	gtcatcagaa	gttaaaccttc	tcctggtttg	ccatggtttt	60
gctgggtgtct	ccactcatgg	ccatgtggga	gctggagaaa	gatgtttatg	ttgttagaggt	120
ggactggcgc	cccgatgccc	ctggagaaac	ggtgaccctc	acctgtgaca	gtcctgaaga	180
agatgacatc	acctggacct	cagaccagag	acgtggagtc	ataggctctg	gaaagaccct	240
gaccatcaact	gtcagagagt	ttctagatgc	tggccaatac	acctgccaca	gaggaggcga	300
gactctgagc	cactcacatc	tgctgctcca	caagaaggaa	aatggattt	ggtccaccga	360
gattttaaaa	aatttcaaaaa	ataagacttt	cctgaagaga	gaagcaccaa	actactccgg	420
acggttcacc	tgctcatggc	tgggcacag	aaacacggac	ttgaagttt	acatcaagag	480
cagcagcagt	tcccctgagt	ctcgccgggt	gacatgtgga	gcagcatctc	tgtctgcaga	540
gaaggtcaca	ctgaacccaaa	gggactacga	gaagtactca	gtggcgtgcc	aggaggacgt	600
cacccgtccca	actgcccggg	agaccctgcc	cattgaactg	gtggtgagg	cccagcagca	660
gaataaatat	gagaactaca	gcaccagctt	cttcatcagg	gacatcatca	aaccggaccc	720
acccaagaac	ctgcaggtga	aacctttgaa	gaactctcg	gtggaggtca	gctggagta	780
ccctgactcc	tggagcactc	cccattccta	cttctccctc	a		821

<210> 12
<211> 268
<212> PRT
<213> Rattus norvegicus

<400> 12

Met	Cys	His	Gln	Lys	Leu	Thr	Phe	Ser	Trp	Phe	Ala	Met	Val	Leu	Leu
1				5			10					15			
Val	Ser	Pro	Leu	Met	Ala	Met	Trp	Glu	Leu	Glu	Lys	Asp	Val	Tyr	Val
							20		25			30			
Val	Glu	Val	Asp	Trp	Arg	Pro	Asp	Ala	Pro	Gly	Glu	Thr	Val	Thr	Leu
							35		40			45			
Thr	Cys	Asp	Ser	Pro	Glu	Glu	Asp	Asp	Ile	Thr	Trp	Thr	Ser	Asp	Gln
							50		55			60			
Arg	Arg	Gly	Val	Ile	Gly	Ser	Gly	Lys	Thr	Leu	Thr	Ile	Thr	Val	Arg
							65		70			75			80
Glu	Phe	Leu	Asp	Ala	Gly	Gln	Tyr	Thr	Cys	His	Arg	Gly	Gly	Glu	Thr
							85		90			95			
Leu	Ser	His	Ser	His	Leu	Leu	Leu	His	Lys	Lys	Glu	Asn	Gly	Ile	Trp
							100		105			110			
Ser	Thr	Glu	Ile	Leu	Lys	Asn	Phe	Lys	Asn	Lys	Thr	Phe	Leu	Lys	Arg
							115		120			125			
Glu	Ala	Pro	Asn	Tyr	Ser	Gly	Arg	Phe	Thr	Cys	Ser	Trp	Leu	Val	His
							130		135			140			
Arg	Asn	Thr	Asp	Leu	Lys	Phe	Asn	Ile	Lys	Ser	Ser	Ser	Ser	Ser	Pro
							145		150			155			160
Glu	Ser	Arg	Ala	Val	Thr	Cys	Gly	Ala	Ala	Ser	Leu	Ser	Ala	Glu	Lys

	165	170	175
Val Thr Leu Asn Gln Arg Asp Tyr Glu Lys Tyr Ser Val Ala Cys Gln			
180	185	190	
Glu Asp Val Thr Cys Pro Thr Ala Glu Glu Thr Leu Pro Ile Glu Leu			
195	200	205	
Val Val Glu Ala Gln Gln Asn Lys Tyr Glu Asn Tyr Ser Thr Ser			
210	215	220	
Phe Phe Ile Arg Asp Ile Ile Lys Pro Asp Pro Pro Lys Asn Leu Gln			
225	230	235	240
Val Lys Pro Leu Lys Asn Ser Gln Val Glu Val Ser Trp Glu Tyr Pro			
245	250		255
Asp Ser Trp Ser Thr Pro His Ser Tyr Phe Ser Leu			
260	265		

<210> 13

<211> 990

<212> DNA

<213> Felis catus

<400> 13

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atggccatat	gggaactgga	aaaaaacgtt	tatgtttag	agttggactg	gcaccctgat	120
gccccccggag	aatgggtggt	cctcacctgt	gacacgcctg	aagaagatga	catcacctgg	180
acctctgacc	agagcagtga	agtccctaggc	tctggtaaaa	ctctgaccat	ccaagtcaaa	240
gaatttgcag	atgctggcca	gtatacctgt	cataaaggag	gcgaggttct	gagccattcg	300
ttcctcctga	tacacaaaaa	ggaagatgga	atttggtcca	ctgatatctt	aaggaaacag	360
aaagaatcca	aaaataagat	ctttctaaaa	tgtgaggcaa	agaattattc	tggacgtttc	420
acctgctggt	ggctgacggc	aatcagtacc	gattgaaat	tcactgtcaa	aagcagcaga	480
ggctcctctg	acccccaagg	ggtgacttgt	ggagcagcga	cactctcagc	agagaaggtc	540
agagtggaca	acagggatta	taagaagtac	acagtggagt	gtcaggaggg	cagtgcctgc	600
ccggctgccc	aggagagcct	accattgaa	gtcgtggtgg	acgctattca	caagctcaag	660
tacgaaaact	acaccagcag	cttcttcatc	agggacatca	tcaaaccgga	cccacccaag	720
aacctgcaac	tgaagccatt	aaaaaaattct	cggcatgtgg	aagtgagctg	ggaataccct	780
gacaccttgg	gcaccccccaca	ttcctacttc	tccttaacat	ttggcgtaca	ggtccagggc	840
aagaacaaca	gagaaaagaa	agacagactc	tccgtggaca	agacctcagc	caaggtcg	900
tgccacaagg	atgccaagat	ccgcgtgcaa	gccagagacc	gctactata	ctcatcctgg	960
agcaactggg	catccgtgtc	ctgcagttag				990

<210> 14

<211> 329

<212> PRT

<213> Felis catus

<400> 14

Met His Pro Gln Gln Leu Val Ile Ala Trp Phe Ser Leu Val Leu Leu						
1	5	10	15			
Ala Pro Pro Leu Met Ala Ile Trp Glu Leu Glu Lys Asn Val Tyr Val						
20	25	30				
Val Glu Leu Asp Trp His Pro Asp Ala Pro Gly Glu Met Val Val Leu						
35	40	45				
Thr Cys Asp Thr Pro Glu Glu Asp Asp Ile Thr Trp Thr Ser Asp Gln						
50	55	60				
Ser Ser Glu Val Leu Gly Ser Gly Lys Thr Leu Thr Ile Gln Val Lys						
65	70	75	80			
Glu Phe Ala Asp Ala Gly Gln Tyr Thr Cys His Lys Gly Gly Glu Val						
85	90	95				
Leu Ser His Ser Phe Leu Leu Ile His Lys Lys Glu Asp Gly Ile Trp						

	100	105	110
Ser	Thr Asp Ile Leu Arg Glu Gln Lys Glu Ser Lys Asn Lys Ile Phe		
	115	120	125
Leu	Lys Cys Glu Ala Lys Asn Tyr Ser Gly Arg Phe Thr Cys Trp Trp		
	130	135	140
Leu	Thr Ala Ile Ser Thr Asp Leu Lys Phe Thr Val Lys Ser Ser Arg		
	145	150	155
Gly	Ser Ser Asp Pro Gln Gly Val Thr Cys Gly Ala Ala Thr Leu Ser		
	165	170	175
Ala	Glu Lys Val Arg Val Asp Asn Arg Asp Tyr Lys Lys Tyr Thr Val		
	180	185	190
Glu	Cys Gln Glu Gly Ser Ala Cys Pro Ala Ala Glu Glu Ser Leu Pro		
	195	200	205
Ile	Glu Val Val Val Asp Ala Ile His Lys Leu Lys Tyr Glu Asn Tyr		
	210	215	220
Thr	Ser Ser Phe Phe Ile Arg Asp Ile Ile Lys Pro Asp Pro Pro Lys		
	225	230	235
Asn	Leu Gln Leu Lys Pro Leu Lys Asn Ser Arg His Val Glu Val Ser		
	245	250	255
Trp	Glu Tyr Pro Asp Thr Trp Ser Thr Pro His Ser Tyr Phe Ser Leu		
	260	265	270
Thr	Phe Gly Val Gln Val Gln Gly Lys Asn Asn Arg Glu Lys Lys Asp		
	275	280	285
Arg	Leu Ser Val Asp Lys Thr Ser Ala Lys Val Val Cys His Lys Asp		
	290	295	300
Ala	Lys Ile Arg Val Gln Ala Arg Asp Arg Tyr Tyr Ser Ser Ser Trp		
	305	310	315
Ser	Asn Trp Ala Ser Val Ser Cys Ser		
	325		

<210> 15
<211> 1006
<212> DNA
<213> Felis catus

<400> 15						
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atggccatat	gggaactgga	aaaaaacgtt	tatgttgttag	agttggactg	gcaccctgat	120
gccccccggag	aaatggtgtt	cctcacctgc	aatactcctg	aagaagatga	catcacctgg	180
acctctgacc	agagcagtga	agtccctaggc	tctggtaaaa	ctctgaccat	ccaagtcaaa	240
gaatttgcag	atgctggcca	gtataccctgt	cataaaggag	gcgagggttct	gagccattcg	300
ttccctcctga	tacacaaaaa	ggaagatgga	atttggtcca	ctgatatatctt	aaggaaacag	360
aaagaatcca	aaaataagat	ctttctaaaa	tgtgaggcaa	agaattatttc	tggacgtttc	420
acctgcttgt	ggctgacggc	aatcagtacc	gatttggaaat	tcactgtcaa	aagcagcaga	480
ggctcctctg	acccccaaga	ggtgacttgt	ggagcagcga	cactctcagc	agagaaggtc	540
agagtggaca	acagggatta	taagaagtac	acagtggagt	gtcaggaggg	cagtgcctgc	600
ccggctgccc	aggagagcct	accattgaa	gtcgtggtg	acgctattca	caagctcaag	660
tacaaaaact	acaccagcag	cttcttcatc	agggacatca	tcaaaccgga	cccacccaag	720
aacctgcAAC	tgaagccatt	aaaaattct	cggcatgtgg	aagttagctg	ggaataccct	780
gacaccttgg	gcaccccaaca	ttcttacttc	tccttaacat	ttggcgtaca	ggtccagggc	840
aagaacaaca	gagaaaagaa	agacagactc	tccgtggaca	agacctcagc	caaggtcgtg	900
tgccacaagg	atgccaagat	ccgcgtgcaa	gccagagacc	gctactatag	ctcatcctgg	960
agcaactggg	catccgtgtc	ctgcagttag	gttccacccc	caggat		1006

<210> 16
<211> 329
<212> PRT

<213> Felis catus

<400> 16

Met His Pro Gln Gln Leu Val Ile Ala Trp Leu Ser Leu Val Leu Leu
1 5 10 15
Ala Pro Pro Leu Met Ala Ile Trp Glu Leu Glu Lys Asn Val Tyr Val
20 25 30
Val Glu Leu Asp Trp His Pro Asp Ala Pro Gly Glu Met Val Val Leu
35 40 45
Thr Cys Asn Thr Pro Glu Glu Asp Asp Ile Thr Trp Thr Ser Asp Gln
50 55 60
Ser Ser Glu Val Leu Gly Ser Gly Lys Thr Leu Thr Ile Gln Val Lys
65 70 75 80
Glu Phe Ala Asp Ala Gly Gln Tyr Thr Cys His Lys Gly Gly Glu Val
85 90 95
Leu Ser His Ser Phe Leu Leu Ile His Lys Lys Glu Asp Gly Ile Trp
100 105 110
Ser Thr Asp Ile Leu Arg Glu Gln Lys Glu Ser Lys Asn Lys Ile Phe
115 120 125
Leu Lys Cys Glu Ala Lys Asn Tyr Ser Gly Arg Phe Thr Cys Trp Trp
130 135 140
Leu Thr Ala Ile Ser Thr Asp Leu Lys Phe Thr Val Lys Ser Ser Arg
145 150 155 160
Gly Ser Ser Asp Pro Gln Glu Val Thr Cys Gly Ala Ala Thr Leu Ser
165 170 175
Ala Glu Lys Val Arg Val Asp Asn Arg Asp Tyr Lys Lys Tyr Thr Val
180 185 190
Glu Cys Gln Glu Gly Ser Ala Cys Pro Ala Ala Glu Glu Ser Leu Pro
195 200 205
Ile Glu Val Val Val Asp Ala Ile His Lys Leu Lys Tyr Glu Asn Tyr
210 215 220
Thr Ser Ser Phe Phe Ile Arg Asp Ile Ile Lys Pro Asp Pro Pro Lys
225 230 235 240
Asn Leu Gln Leu Lys Pro Leu Lys Asn Ser Arg His Val Glu Val Ser
245 250 255
Trp Glu Tyr Pro Asp Thr Trp Ser Thr Pro His Ser Tyr Phe Ser Leu
260 265 270
Thr Phe Gly Val Gln Val Gln Gly Lys Asn Asn Arg Glu Lys Lys Asp
275 280 285
Arg Leu Ser Val Asp Lys Thr Ser Ala Lys Val Val Cys His Lys Asp
290 295 300
Ala Lys Ile Arg Val Gln Ala Arg Asp Arg Tyr Tyr Ser Ser Ser Trp
305 310 315 320
Ser Asn Trp Ala Ser Val Ser Cys Ser
325

<210> 17

<211> 1058

<212> DNA

<213> Equus caballus

<400> 17

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atggccatat gggacttggaa gaaagatgtg tatgttgttag aattggattt gtaccctgtat
gcccttggag aaatggttgtt cctcacctgc aataccctgt aagaagaagg catcacctgg
acctcgcccc agagcaatga ggtcttaggc tctggaaaa ccttgaccat ccaagtcaaa
gagtttggag atgctggctg gtacacctgt cacaaaggag gcgaggttct gagcattct
60
120
180
240
300

cacctgctgc	ttcacaagaa	ggaagatgga	atttggtcca	ctgacatttt	aaaagaccag	360
aaagaatcca	aaaataagac	ctttctaaaa	tgtgaggcaa	agaattattc	cggacgtttc	420
acatgctgg	ggctgacagc	aatcagtact	gattgaaat	tcagtgtcaa	aagcagcaga	480
ggttccctcg	accccccagg	ggtgacgtgt	ggagcagcga	cactctccgc	agagagggtc	540
agcgtggacg	acagggagta	taagaagtac	acggtgaggt	gtcaggaggg	cagtgcctgc	600
ccggccgccc	aggagagcct	gcccatttag	atcgtgttgg	atgctgttca	caagctcaag	660
tatgaaaact	acaccagcgg	cttcttcata	agggacatca	tcaaaccaga	cccacccaag	720
aacctgcagc	tgaagccatt	aaagaattct	cggcaggtgg	aggtcagctg	ggagtacccc	780
gagacctgga	gcacccccaca	ttcctacttc	tccctgacat	tctctattca	ggtccaggc	840
aagaacaaga	aggaaaggaa	agacagactc	ttcatggatg	agacttcagc	cacagtacaca	900
tgccacaagg	atggccagat	ccgtgtccaa	gccaggacc	gctactacag	ctcatcctgg	960
agcgaatggg	catccgtatc	ctgcagttag	ggatgcagac	tcagggcagcc	caggccagac	1020
ctgaacactc	agtgtaccca	ggttctaacc	tcagtatg			1058

<210> 18

<211> 329

<212> PRT

<213> Equus caballus

<400> 18

Met	Cys	His	Gln	Trp	Leu	Val	Leu	Ser	Trp	Phe	Ser	Leu	Val	Leu	Leu	
1				5					10					15		
Ala	Ser	Pro	Leu	Met	Ala	Ile	Trp	Glu	Leu	Glu	Lys	Asp	Val	Tyr	Val	
					20				25					30		
Val	Glu	Leu	Asp	Trp	Tyr	Pro	Asp	Ala	Pro	Gly	Glu	Met	Val	Val	Leu	
					35				40					45		
Thr	Cys	Asn	Thr	Pro	Glu	Glu	Gly	Ile	Thr	Trp	Thr	Ser	Ala	Gln		
					50				55					60		
Ser	Asn	Glu	Val	Leu	Gly	Ser	Gly	Lys	Thr	Leu	Thr	Ile	Gln	Val	Lys	
					65				70					75		80
Glu	Phe	Gly	Asp	Ala	Gly	Trp	Tyr	Thr	Cys	His	Lys	Gly	Gly	Glu	Val	
					85				90					95		
Leu	Ser	His	Ser	His	Leu	Leu	Leu	His	Lys	Lys	Glu	Asp	Gly	Ile	Trp	
					100				105					110		
Ser	Thr	Asp	Ile	Leu	Lys	Asp	Gln	Lys	Glu	Ser	Lys	Asn	Lys	Thr	Phe	
					115				120					125		
Leu	Lys	Cys	Glu	Ala	Lys	Asn	Tyr	Ser	Gly	Arg	Phe	Thr	Cys	Trp	Trp	
					130				135					140		
Leu	Thr	Ala	Ile	Ser	Thr	Asp	Leu	Lys	Phe	Ser	Val	Lys	Ser	Ser	Arg	
					145				150					155		160
Gly	Ser	Ser	Asp	Pro	Arg	Gly	Val	Thr	Cys	Gly	Ala	Ala	Thr	Leu	Ser	
					165				170					175		
Ala	Glu	Arg	Val	Ser	Val	Asp	Asp	Arg	Glu	Tyr	Lys	Lys	Tyr	Thr	Val	
					180				185					190		
Glu	Cys	Gln	Glu	Gly	Ser	Ala	Cys	Pro	Ala	Ala	Glu	Glu	Ser	Leu	Pro	
					195				200					205		
Ile	Glu	Ile	Val	Val	Asp	Ala	Val	His	Lys	Leu	Lys	Tyr	Glu	Asn	Tyr	
					210				215					220		
Thr	Ser	Gly	Phe	Phe	Ile	Arg	Asp	Ile	Ile	Lys	Pro	Asp	Pro	Pro	Lys	
					225				230					235		240
Asn	Leu	Gln	Leu	Lys	Pro	Leu	Lys	Asn	Ser	Arg	Gln	Val	Glu	Val	Ser	
					245				250					255		
Trp	Glu	Tyr	Pro	Glu	Thr	Trp	Ser	Thr	Pro	His	Ser	Tyr	Phe	Ser	Leu	
					260				265					270		
Thr	Phe	Ser	Ile	Gln	Val	Gln	Gly	Lys	Asn	Lys	Lys	Glu	Arg	Lys	Asp	
					275				280					285		
Arg	Leu	Phe	Met	Asp	Glu	Thr	Ser	Ala	Thr	Val	Thr	Cys	His	Lys	Asp	

290	295	300
Gly Gln Ile Arg Val Gln Ala Arg Asp Arg Tyr Tyr Ser Ser Ser Trp		
305	310	315
Ser Glu Trp Ala Ser Val Ser Cys Ser		
	325	

<210> 19
<211> 1399
<212> DNA
<213> Homo sapiens

<400> 19		
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aagaaaagatg tttatgtcgt agaattggat tggtatccgg atgcccctgg agaaaatggtg	180	
gtcctcacct gtgacacccc tgaagaagat ggtatcacct ggaccttggg ccagagcagt	240	
gaggcttttag gctctggcaa aaccctgacc atccaagtca aagagtttg agatgtggc	300	
cagtagcacct gtcacaaagg aggcgagggt ctaagccatt cgctcctgct gcttcacaaa	360	
aaggaagatg gaatttggtc cactgatatt ttaaaggacc agaaaagaacc caaaaataag	420	
acctttctaa gatgcgaggc caagaattat tctggacgtt tcacctgctg gtggctgacg	480	
acaatcaga ctgatttgac attcagtgtc aaaagcagca gaggctttc tgaccccaa	540	
gggggtacgt gcggagctgc tacactctt gcagagagag tcagaggggca caacaaggag	600	
tatgagtact cagtgagggt ccaggaggac agtgcctgcc cagctgctga ggagagtctg	660	
cccattgagg tcatggtggg tgccgttac aagctcaagt atgaaaacta caccacgc	720	
ttcttcatca gggacatcat caaacctgac ccacccaaaga acttgcagct gaagccatta	780	
aagaattctc ggcaggtggg ggtcagctgg gagtaccctg acacctggag tactccatat	840	
tcctacttct ccctgacatt ctgcgtttag gtccaggggca agagcaagag agaaaaagaaa	900	
gatagagtct tcacggacaa gacctcagcc acggcatct gccgcacaaa tgccagcatt	960	
agcgtgcggg cccaggaccg ctactatagc tcatcttgg gccaatgggc atctgtgccc	1020	
tgcagtagg ttctgatcca ggtaaaaat ttggaggaaa agtggaaagat attaagcaaa	1080	
atgtttaaag acacaacgga atagacccaa aaagataatt tctatctgat ttgctttaaa	1140	
acgtttttt aggatcacaa tgatatctt gctgtatgg tatagttga tgctaaatgc	1200	
tcattgaaac aatcagctaa tttatgtata gatttccag ctctcaagtt gccatggcc	1260	
ttcatgctat ttaaatatTTT aagtaattt tgtattttt agtataattac tgttattaa	1320	
cgtttgtctg ccaggatgtt tggaatgttt catactctt tgacctgatc catcaggatc	1380	
agtccctatt atgcaaaaat	1399	

<210> 20
<211> 328
<212> PRT
<213> Homo sapiens

<400> 20		
Met Cys His Gln Gln Leu Val Ile Ser Trp Phe Ser Leu Val Phe Leu		
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Ala Ser Pro Leu Val Ala Ile Trp Glu Leu Lys Lys Asp Val Tyr Val		
20 25 30		
Val Glu Leu Asp Trp Tyr Pro Asp Ala Pro Gly Glu Met Val Val Leu		
35 40 45		
Thr Cys Asp Thr Pro Glu Glu Asp Gly Ile Thr Trp Thr Leu Asp Gln		
50 55 60		
Ser Ser Glu Val Leu Gly Ser Gly Lys Thr Leu Thr Ile Gln Val Lys		
65 70 75 80		
Glu Phe Gly Asp Ala Gly Gln Tyr Thr Cys His Lys Gly Gly Glu Val		
85 90 95		
Leu Ser His Ser Leu Leu Leu His Lys Lys Glu Asp Gly Ile Trp		
100 105 110		

Ser Thr Asp Ile Leu Lys Asp Gln Lys Glu Pro Lys Asn Lys Thr Phe
 115 120 125
 Leu Arg Cys Glu Ala Lys Asn Tyr Ser Gly Arg Phe Thr Cys Trp Trp
 130 135 140
 Leu Thr Thr Ile Ser Thr Asp Leu Thr Phe Ser Val Lys Ser Ser Arg
 145 150 155 160
 Gly Ser Ser Asp Pro Gln Gly Val Thr Cys Gly Ala Ala Thr Leu Ser
 165 170 175
 Ala Glu Arg Val Arg Gly Asp Asn Lys Glu Tyr Glu Tyr Ser Val Glu
 180 185 190
 Cys Gln Glu Asp Ser Ala Cys Pro Ala Ala Glu Glu Ser Leu Pro Ile
 195 200 205
 Glu Val Met Val Asp Ala Val His Lys Leu Lys Tyr Glu Asn Tyr Thr
 210 215 220
 Ser Ser Phe Phe Ile Arg Asp Ile Ile Lys Pro Asp Pro Pro Lys Asn
 225 230 235 240
 Leu Gln Leu Lys Pro Leu Lys Asn Ser Arg Gln Val Glu Val Ser Trp
 245 250 255
 Glu Tyr Pro Asp Thr Trp Ser Thr Pro His Ser Tyr Phe Ser Leu Thr
 260 265 270
 Phe Cys Val Gln Val Gln Gly Lys Ser Lys Arg Glu Lys Lys Asp Arg
 275 280 285
 Val Phe Thr Asp Lys Thr Ser Ala Thr Val Ile Cys Arg Lys Asn Ala
 290 295 300
 Ser Ile Ser Val Arg Ala Gln Asp Arg Tyr Tyr Ser Ser Ser Trp Ser
 305 310 315 320
 Glu Trp Ala Ser Val Pro Cys Ser
 325

<210> 21
 <211> 1012
 <212> DNA
 <213> Capra hircus

<400> 21

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gctcctggag	aaacagtgg	cctcacgtgt	gacactcctg	agaagacgg	catcacctgg	180
acctcagacc	agagcagtga	ggtcctgggc	tctggaaaa	ccttgaccat	ccaagtcaaa	240
gagtttggag	atgctggca	gtacacctgt	cacaaaggag	gcgagggtct	gagtcgttca	300
ctcctcctgc	ttcacaaaaa	ggaagatgg	atttggtcca	ctgatatttt	aaaggatcag	360
aaagaaccca	aagctaagag	tttttaaaa	tgtgaggcaa	aggattattt	tggacacttc	420
acctgcttgt	ggctgacagc	aatcagtact	aatctgaaat	tcagtgtcaa	aagcagcaga	480
ggctcctctg	accccccgg	ggtgacgtgc	ggagcagcgt	cactctcagc	agagaaggtc	540
agcatggacc	acagggagta	taacaagtac	acagtggagt	gtcaggaggg	cagtgcctgc	600
ccggccgccc	aggagagcct	gcccatttag	gtcgtgatgg	aagctgtgca	caagctcaag	660
tatgaaaaact	acaccagcag	cttcttcatc	agggacatca	tcaaaccaga	cccacccaag	720
aacctgcAAC	tgagaccact	aaagaattct	cgccaggtgg	aggtcagctg	ggagtaccct	780
gacacgtgga	gcaccccaaca	ttcctacttc	tccctgacgt	tttgcgttca	ggtccaggga	840
aagaacaaga	gagaaaagaa	actcttcacg	gaccaaacct	cagccaaagt	cacatgccac	900
aaggatgcca	acatccgtgt	gcaagccccgg	gaccgctact	acagctcatt	ctggagtgaa	960
tgggcatctg	tgtcctgcag	ttaggttcta	acctcagtat	gaaacctcag	ag	1012

<210> 22
 <211> 327
 <212> PRT
 <213> Capra hircus

<400> 22

Met	His	Pro	Gln	Gln	Leu	Val	Val	Ser	Trp	Phe	Ser	Leu	Val	Leu	Leu
1					5				10					15	
Ala	Ser	Pro	Ile	Val	Ala	Ile	Trp	Glu	Leu	Glu	Lys	Asn	Val	Tyr	Val
			20					25					30		
Val	Glu	Leu	Asp	Trp	Tyr	Pro	Asn	Ala	Pro	Gly	Glu	Thr	Val	Val	Leu
			35					40				45			
Thr	Cys	Asp	Thr	Pro	Glu	Glu	Asp	Gly	Ile	Thr	Trp	Thr	Ser	Asp	Gln
			50					55			60				
Ser	Ser	Glu	Val	Leu	Gly	Ser	Gly	Lys	Thr	Leu	Thr	Ile	Gln	Val	Lys
			65					70			75		80		
Glu	Phe	Gly	Asp	Ala	Gly	Gln	Tyr	Thr	Cys	His	Lys	Gly	Gly	Glu	Val
			85					90				95			
Leu	Ser	Arg	Ser	Leu	Leu	Leu	Leu	His	Lys	Lys	Glu	Asp	Gly	Ile	Trp
			100					105				110			
Ser	Thr	Asp	Ile	Leu	Lys	Asp	Gln	Lys	Glu	Pro	Lys	Ala	Lys	Ser	Phe
			115					120			125				
Leu	Lys	Cys	Glu	Ala	Lys	Asp	Tyr	Ser	Gly	His	Phe	Thr	Cys	Ser	Trp
			130					135			140				
Leu	Thr	Ala	Ile	Ser	Thr	Asn	Leu	Lys	Phe	Ser	Val	Lys	Ser	Ser	Arg
			145					150			155		160		
Gly	Ser	Ser	Asp	Pro	Arg	Gly	Val	Thr	Cys	Gly	Ala	Ala	Ser	Leu	Ser
			165					170			175				
Ala	Glu	Lys	Val	Ser	Met	Asp	His	Arg	Glu	Tyr	Asn	Lys	Tyr	Thr	Val
			180					185			190				
Glu	Cys	Gln	Glu	Gly	Ser	Ala	Cys	Pro	Ala	Ala	Glu	Glu	Ser	Leu	Pro
			195					200			205				
Ile	Glu	Val	Val	Met	Glu	Ala	Val	His	Lys	Leu	Lys	Tyr	Glu	Asn	Tyr
			210					215			220				
Thr	Ser	Ser	Phe	Phe	Ile	Arg	Asp	Ile	Ile	Lys	Pro	Asp	Pro	Pro	Lys
			225					230			235		240		
Asn	Leu	Gln	Leu	Arg	Pro	Leu	Lys	Asn	Ser	Arg	Gln	Val	Glu	Val	Ser
			245					250			255				
Trp	Glu	Tyr	Pro	Asp	Thr	Trp	Ser	Thr	Pro	His	Ser	Tyr	Phe	Ser	Leu
			260					265			270				
Thr	Phe	Cys	Val	Gln	Val	Gln	Gly	Lys	Asn	Lys	Arg	Glu	Lys	Lys	Leu
			275					280			285				
Phe	Thr	Asp	Gln	Thr	Ser	Ala	Lys	Val	Thr	Cys	His	Lys	Asp	Ala	Asn
			290					295			300				
Ile	Arg	Val	Gln	Ala	Arg	Asp	Arg	Tyr	Tyr	Ser	Ser	Phe	Trp	Ser	Glu
			305					310			315		320		
Trp	Ala	Ser	Val	Ser	Cys	Ser									
			325												

<210> 23

<211> 1080

<212> DNA

<213> Macaca mulatta

<400> 23

gccccagagca	agatgtgtca	ccagcagctg	gtcatctctt	ggttttccct	ggttttcttg	60
gcatctcccc	tcatggccat	atgggaactg	aagaaagacg	tttatgttgt	agaattggac	120
tggtaccgg	atgcccctgg	agaaaatggt	gtcctcacct	gtgacacccc	tgaagaagat	180
ggtatcacct	ggaccttgg	ccagagtgg	gaggtcttag	gctctggcaa	aaccctgacc	240
atccaagtca	aagagtttgg	agatgctggc	cagtacacct	gtcacaagg	aggcgaggct	300
ctaagccatt	cactcctgct	gcttcacaaa	aaggaagatg	gaatttggtc	cactgatgt	360

ttaaaggacc	agaaaagaacc	caaaaataag	acctttctaa	gatgtgaggc	caaaaattat	420
tctggacgtt	tcacactgctg	gtggctgacg	acaatcagta	ctgatctgac	attcagtgtc	480
aaaagcagca	gaggctcttc	taaccccaa	gggggtgacgt	gtggagccgt	tacactctct	540
gcagagaggg	tcagagggga	caataaggag	tatgagtact	cagtggagtg	ccaggaggac	600
agtgcctgcc	cagccgctga	ggagaggctg	cccattgagg	tcatggtgga	tgccattcac	660
aagctcaagt	atgaaaacta	caccagcagc	ttcttcatca	gggacatcat	caaaccgac	720
ccacccaaga	acttgcagct	gaagccatta	aagaattctc	ggcaggtgga	ggtcagctgg	780
gagtaccctg	acacctggag	tactccacat	tcctacttct	ccctgacatt	ctgcatccag	840
gtccaggcga	agagcaagag	agaaaaagaaa	gatagaatct	tcacagacaa	gacctcagcc	900
acggtcatct	gccgcaaaaa	tgccagcttt	agcgtgcagg	cccaggaccg	ctactatagc	960
tcatcttgg	g c g a a t g g g c	atctgtgccc	tgcagttagg	ttgtgatccc	aggatgaaaa	1020
attggaggaa	aagtagaaga	tattaaccaa	aacgttaaa	gacacaacgg	aatagaccca	1080

<210> 24
<211> 328
<212> PRT
<213> Macaca mulatta

<400> 24						
Met Cys His Gln Gln Leu Val Ile Ser Trp Phe Ser Leu Val Phe Leu						
1	5	10	15			
Ala Ser Pro Leu Met Ala Ile Trp Glu Leu Lys Lys Asp Val Tyr Val						
20	25	30				
Val Glu Leu Asp Trp Tyr Pro Asp Ala Pro Gly Glu Met Val Val Leu						
35	40	45				
Thr Cys Asp Thr Pro Glu Glu Asp Gly Ile Thr Trp Thr Leu Asp Gln						
50	55	60				
Ser Gly Glu Val Leu Gly Ser Gly Lys Thr Leu Thr Ile Gln Val Lys						
65	70	75	80			
Glu Phe Gly Asp Ala Gly Gln Tyr Thr Cys His Lys Gly Gly Glu Ala						
85	90	95				
Leu Ser His Ser Leu Leu Leu His Lys Lys Glu Asp Gly Ile Trp						
100	105	110				
Ser Thr Asp Val Leu Lys Asp Gln Lys Glu Pro Lys Asn Lys Thr Phe						
115	120	125				
Leu Arg Cys Glu Ala Lys Asn Tyr Ser Gly Arg Phe Thr Cys Trp Trp						
130	135	140				
Leu Thr Thr Ile Ser Thr Asp Leu Thr Phe Ser Val Lys Ser Ser Arg						
145	150	155	160			
Gly Ser Ser Asn Pro Gln Gly Val Thr Cys Gly Ala Val Thr Leu Ser						
165	170	175				
Ala Glu Arg Val Arg Gly Asp Asn Lys Glu Tyr Glu Tyr Ser Val Glu						
180	185	190				
Cys Gln Glu Asp Ser Ala Cys Pro Ala Ala Glu Glu Arg Leu Pro Ile						
195	200	205				
Glu Val Met Val Asp Ala Ile His Lys Leu Lys Tyr Glu Asn Tyr Thr						
210	215	220				
Ser Ser Phe Phe Ile Arg Asp Ile Ile Lys Pro Asp Pro Pro Lys Asn						
225	230	235	240			
Leu Gln Leu Lys Pro Leu Lys Asn Ser Arg Gln Val Glu Val Ser Trp						
245	250	255				
Glu Tyr Pro Asp Thr Trp Ser Thr Pro His Ser Tyr Phe Ser Leu Thr						
260	265	270				
Phe Cys Ile Gln Val Gln Gly Lys Ser Lys Arg Glu Lys Lys Asp Arg						
275	280	285				
Ile Phe Thr Asp Lys Thr Ser Ala Thr Val Ile Cys Arg Lys Asn Ala						
290	295	300				

Ser Phe Ser Val Gln Ala Gln Asp Arg Tyr Tyr Ser Ser Ser Trp Ser
 305 310 315 320
 Glu Trp Ala Ser Val Pro Cys Ser
 325

<210> 25

<211> 1012

<212> DNA

<213> Bos taurus

<400> 25

atgcaccctc	agcagtttgt	cgttccctgg	ttttccctgg	tttgctggc	atctcccatc	60
gtggccatgt	ggaaactgga	aaaaatgtt	tatgttgtag	aattggattt	gtatccctgat	120
gctccctggag	aaacagtttgt	cctcacatgt	gacactcctg	aagaagatgg	catcacctgg	180
acctcagacc	agagcagtga	ggtcttgggc	tctggaaaaa	ccttgaccat	ccaagtcaaa	240
gagtttggag	atgctggca	gtacacctgt	cacaaaggag	gcgaggctct	gagtgcgtca	300
ctcctccctgc	tgcacaaaaa	ggaagatgga	atttggtcca	ctgatatttt	aaaggatcag	360
aaagaaccca	aagctaagag	tttttaaaa	tgtgaggcaa	aggattattc	tggacacttc	420
acctgcttgt	ggctgacagc	aatcagtact	gatttggaaat	tcagtgtcaa	aagcagcaga	480
ggctccctcg	acccccgagg	ggtgacgtgc	ggagcagcgt	tgctctcagc	agagaaggc	540
agcttggagc	acagggagta	taacaagtac	acagtggagt	gtcaggaggg	cagcgcctgc	600
ccagccgctg	aggagagcct	gcttatttag	gtcgtggtag	aagctgtgca	caagctcaag	660
tataaaaact	acaccaggcag	cttcttcatac	agggacatca	tcaaaccaga	cccacccaag	720
aacctgcaac	tgagaccatt	aaagaattct	cggcaggtgg	aggtcagctg	ggagtaccct	780
gacacgtgga	gcaccccgca	ttcctacttc	tccctgacgt	tttggttca	gttccaggga	840
aagaacaaga	gagaaaagaa	actcttcatg	gaccaaacct	cagccaaagt	cacatgccac	900
aaggatgcca	acgtccgcgt	gcaagcccg	gaccgctact	acagctcatt	ctggagtgaa	960
tggcatctg	tgtcctgcag	ttaggttcta	acctcagtat	gaaacctcag	ag	1012

<210> 26

<211> 327

<212> PRT

<213> Bos taurus

<400> 26

Met His Pro Gln Gln	Leu Val Val Ser	Trp Phe Ser	Leu Val Leu Leu			
1	5	10	15			
Ala Ser Pro Ile Val Ala Met	Trp Glu Leu Glu Lys	Asn Val Tyr Val				
20	25	30				
Val Glu Leu Asp Trp Tyr Pro Asp	Ala Pro Gly Glu Thr	Val Val Leu				
35	40	45				
Thr Cys Asp Thr Pro Glu Glu Asp	Gly Ile Thr Trp Thr	Ser Asp Gln				
50	55	60				
Ser Ser Glu Val Leu Gly Ser	Gly Lys Thr Leu Thr	Ile Gln Val Lys				
65	70	75	80			
Glu Phe Gly Asp Ala Gly Gln	Tyr Thr Cys His Lys	Gly Glu Ala				
85	90	95				
Leu Ser Arg Ser Leu Leu Leu	His Lys Lys Glu Asp	Gly Ile Trp				
100	105	110				
Ser Thr Asp Ile Leu Lys Asp	Gln Lys Glu Pro Lys	Ala Lys Ser Phe				
115	120	125				
Leu Lys Cys Glu Ala Lys Asp	Tyr Ser Gly His Phe	Thr Cys Trp Trp				
130	135	140				
Leu Thr Ala Ile Ser Thr Asp	Leu Lys Phe Ser Val	Lys Ser Ser Arg				
145	150	155	160			
Gly Ser Ser Asp Pro Arg Gly	Val Thr Cys Gly Ala	Ala Leu Leu Ser				
165	170	175				

Ala Glu Lys Val Ser Leu Glu His Arg Glu Tyr Asn Lys Tyr Thr Val
 180 185 190
 Glu Cys Gln Glu Gly Ser Ala Cys Pro Ala Ala Glu Glu Ser Leu Leu
 195 200 205
 Ile Glu Val Val Val Glu Ala Val His Lys Leu Lys Tyr Glu Asn Tyr
 210 215 220
 Thr Ser Ser Phe Phe Ile Arg Asp Ile Ile Lys Pro Asp Pro Pro Lys
 225 230 235 240
 Asn Leu Gln Leu Arg Pro Leu Lys Asn Ser Arg Gln Val Glu Val Ser
 245 250 255
 Trp Glu Tyr Pro Asp Thr Trp Ser Thr Pro His Ser Tyr Phe Ser Leu
 260 265 270
 Thr Phe Cys Val Gln Val Gln Gly Lys Asn Lys Arg Glu Lys Lys Leu
 275 280 285
 Phe Met Asp Gln Thr Ser Ala Lys Val Thr Cys His Lys Asp Ala Asn
 290 295 300
 Val Arg Val Gln Ala Arg Asp Arg Tyr Tyr Ser Ser Phe Trp Ser Glu
 305 310 315 320
 Trp Ala Ser Val Ser Cys Ser
 325

<210> 27
 <211> 993
 <212> DNA
 <213> Cervus elaphus

<400> 27
 atgcaccctc agcagtttgt cgtttcctgg ttttcctgg ttttgctgac atctccatt
 gtggccatat gggaaacttggaa gaaaaatgtt tatgttgttag aattggattt gatatcctgat
 gcttcctggag aaacgggttgt cctcagggtgt gacactcctg aagaagacggg tatcacctgg
 acctcagacc agagcagtga ggtcttgggc tctggcaaaa ccttgaccgt ccaagtcaaa
 gagtttggag atgctgggca gtacacctgt cacaaggag gcgaggttct gagtcgttca
 ctccttcctgc tgcacaaaaa ggaagatggaa atttggtcta ctgatatttt aaaggatcag
 aaagaaccca aagccaagag ttttttaaaa tgtgaggcaa aggattattc tggacacttc
 acctgcttgtt ggctgacagc aatcagttact gatggaaat tcagtgtaa aagcagcaga
 ggcttccttg accccccgagg ggtgacgtgc ggagcagcgt cgctctcaac agagaaggc
 atttgtggacc acagggagta taagaagtac acagtggagt gtcaagaggg cagcgcctgc
 ccggccgcgcg aggagagcct gccatttggag gtcgttagtgg aagctgtgca caagctcaag
 tatgaaaaact acaccagcag cttcttcattc agggacatca tcaaaccaga cccacccaag
 aacctgcaac tgagaccatt aaagaattct cggcagggtgg aggtcagctg ggagtaccct
 gacacgtgga gcacccca ttccttacttc tccctgacgt tttgtgttca ggtccaggga
 aagaacaaga gaaaaagaa acttttcatg gaccaaacct cagccaaagt cacgtgtcac
 aaggatgccca gcatccgcgt gcaagcccg gaccgctact acaactcatt ctggagtgaa
 tgggcattctg tgcctgcag ttagtgcata acc 993

<210> 28
 <211> 327
 <212> PRT
 <213> Cervus elaphus

<400> 28
 Met His Pro Gln Gln Leu Val Val Ser Trp Phe Ser Leu Val Leu
 1 5 10 15
 Thr Ser Pro Ile Val Ala Ile Trp Glu Leu Glu Lys Asn Val Tyr Val
 20 25 30
 Val Glu Leu Asp Trp Tyr Pro Asp Ala Pro Gly Glu Thr Val Val Leu
 35 40 45

Arg Cys Asp Thr Pro Glu Glu Asp Gly Ile Thr Trp Thr Ser Asp Gln
 50 55 60
 Ser Ser Glu Val Leu Gly Ser Gly Lys Thr Leu Thr Val Gln Val Lys
 65 70 75 80
 Glu Phe Gly Asp Ala Gly Gln Tyr Thr Cys His Lys Gly Gly Glu Val
 85 90 95
 Leu Ser Arg Ser Leu Leu Leu His Lys Lys Glu Asp Gly Ile Trp
 100 105 110
 Ser Thr Asp Ile Leu Lys Asp Gln Lys Glu Pro Lys Ala Lys Ser Phe
 115 120 125
 Leu Lys Cys Glu Ala Lys Asp Tyr Ser Gly His Phe Thr Cys Trp Trp
 130 135 140
 Leu Thr Ala Ile Ser Thr Asp Leu Lys Phe Ser Val Lys Ser Ser Arg
 145 150 155 160
 Gly Ser Ser Asp Pro Arg Gly Val Thr Cys Gly Ala Ala Ser Leu Ser
 165 170 175
 Thr Glu Lys Val Ile Val Asp His Arg Glu Tyr Lys Lys Tyr Thr Val
 180 185 190
 Glu Cys Gln Glu Gly Ser Ala Cys Pro Ala Ala Glu Glu Ser Leu Pro
 195 200 205
 Ile Glu Val Val Val Glu Ala Val His Lys Leu Lys Tyr Glu Asn Tyr
 210 215 220
 Thr Ser Ser Phe Phe Ile Arg Asp Ile Ile Lys Pro Asp Pro Pro Lys
 225 230 235 240
 Asn Leu Gln Leu Arg Pro Leu Lys Asn Ser Arg Gln Val Glu Val Ser
 245 250 255
 Trp Glu Tyr Pro Asp Thr Trp Ser Thr Pro His Ser Tyr Phe Ser Leu
 260 265 270
 Thr Phe Cys Val Gln Val Gln Gly Lys Asn Lys Arg Glu Lys Lys Leu
 275 280 285
 Phe Met Asp Gln Thr Ser Ala Lys Val Thr Cys His Lys Asp Ala Ser
 290 295 300
 Ile Arg Val Gln Ala Arg Asp Arg Tyr Tyr Asn Ser Phe Trp Ser Glu
 305 310 315 320
 Trp Ala Ser Val Ser Cys Ser
 325

<210> 29
 <211> 984
 <212> DNA
 <213> Ovis aries

<400> 29

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gtggccatat	gggaactgga	aaaaaatgtt	tatgttgtag	aattggattt	gtatcctaataat	120
gctccctggag	aaacagtgg	cctcacgtgt	gacactcctg	aaaagacgg	catcacctgg	180
acctcagacc	agagcagtga	ggtcctgggc	tctggcaaaa	cottgaccat	ccaagtcaaa	240
gagtttggag	atgctgggca	gtacacctgt	cacaaaggag	gcgaggttct	gagtcgttca	300
ctcctcctgc	tgcacaaaaa	ggaagatgga	atttggtcca	ctgatatttt	aaaggatcag	360
aaagaaccca	aagctaagag	tttttaaaaa	tgtgaggcaa	aggattttt	tggacacttc	420
acctgctcg	ggctgacagc	aatcagtact	aatctgaaat	tcagtgtcaa	aagcagcaga	480
ggctcctctg	accccccggagg	ggtgacgtgc	ggagcagcgt	ccctctcagc	agagaaggtc	540
agcatggacc	acagggagta	taacaagtac	acagtggagt	gtcaggaggg	cagtgcctgc	600
ccggccgccc	aggagagcct	gcccatggag	gtcgtgtatgg	aagctgtgca	caagctcaag	660
tatgaaaact	acaccagcag	cttcttcatc	agggacatca	tcaaaccaga	cccacccaag	720
aacctgcaac	tgagaccact	aaagaattct	cggcaggtgg	aagtctgctg	ggagtaccct	780
gacacgtgga	gcaccccaaca	ttcctacttc	tccctgacgt	tttgggttca	ggtccaggga	840

aagaacaaga gagaaaagaa actttcaca gaccaaacct cagccaaagt cacatgccac	900
aaggatgcca acatccgcgt gcaagccgg gaccgctact acagctcatt ctggagtgaa	960
tggcatctg tgcctgcag ttag	984

<210> 30
<211> 327
<212> PRT
<213> Ovis aries

<400> 30	
Met His Pro Gln Gln Leu Val Val Ser Trp Phe Ser Leu Val Leu	
1 5 10 15	
Ala Ser Pro Ile Val Ala Ile Trp Glu Leu Glu Lys Asn Val Tyr Val	
20 25 30	
Val Glu Leu Asp Trp Tyr Pro Asn Ala Pro Gly Glu Thr Val Val Leu	
35 40 45	
Thr Cys Asp Thr Pro Glu Glu Asp Gly Ile Thr Trp Thr Ser Asp Gln	
50 55 60	
Ser Ser Glu Val Leu Gly Ser Gly Lys Thr Leu Thr Ile Gln Val Lys	
65 70 75 80	
Glu Phe Gly Asp Ala Gly Gln Tyr Thr Cys His Lys Gly Glu Val	
85 90 95	
Leu Ser Arg Ser Leu Leu Leu His Lys Lys Glu Asp Gly Ile Trp	
100 105 110	
Ser Thr Asp Ile Leu Lys Asp Gln Lys Glu Pro Lys Ala Lys Ser Phe	
115 120 125	
Leu Lys Cys Glu Ala Lys Asp Tyr Ser Gly His Phe Thr Cys Ser Trp	
130 135 140	
Leu Thr Ala Ile Ser Thr Asn Leu Lys Phe Ser Val Lys Ser Ser Arg	
145 150 155 160	
Gly Ser Ser Asp Pro Arg Gly Val Thr Cys Gly Ala Ala Ser Leu Ser	
165 170 175	
Ala Glu Lys Val Ser Met Asp His Arg Glu Tyr Asn Lys Tyr Thr Val	
180 185 190	
Glu Cys Gln Glu Gly Ser Ala Cys Pro Ala Ala Glu Glu Ser Leu Pro	
195 200 205	
Ile Glu Val Val Met Glu Ala Val His Lys Leu Lys Tyr Glu Asn Tyr	
210 215 220	
Thr Ser Ser Phe Phe Ile Arg Asp Ile Ile Lys Pro Asp Pro Pro Lys	
225 230 235 240	
Asn Leu Gln Leu Arg Pro Leu Lys Asn Ser Arg Gln Val Glu Val Ser	
245 250 255	
Trp Glu Tyr Pro Asp Thr Trp Ser Thr Pro His Ser Tyr Phe Ser Leu	
260 265 270	
Thr Phe Cys Val Gln Val Gln Gly Lys Asn Lys Arg Glu Lys Lys Leu	
275 280 285	
Phe Thr Asp Gln Thr Ser Ala Lys Val Thr Cys His Lys Asp Ala Asn	
290 295 300	
Ile Arg Val Gln Ala Arg Asp Arg Tyr Tyr Ser Ser Phe Trp Ser Glu	
305 310 315 320	
Trp Ala Ser Val Ser Cys Ser	
325	

<210> 31
<211> 1015
<212> DNA
<213> Canis familiaris

<400> 31

atgcatcctc	agcagtttgt	catctcctgg	tttccctcg	tttgctggc	gtcttcctc	60
atgaccatat	ggaaactgga	gaaagatgtt	tatgtttag	agttggactg	gcacctgat	120
gccccccgag	aatgggttgt	cctcacctgc	cataccctg	aagaagatga	catcaattgg	180
acctcagcgc	agagcagtga	agtccatgt	tctggtaaaa	ctctgaccat	ccaagtcaaa	240
gaatttggag	atgctggcca	gtatacctgc	cataaaggag	gcaaggttct	gagccgctca	300
ctcctgttga	ttcacaaaaaa	agaagatgga	atttggtcca	ctgatatctt	aaaggaacag	360
aaagaatcca	aaaataagat	cttctgaaa	tgtgaggcaa	agaattatttc	tggacgtttc	420
acatgcttgt	ggctgacggc	aatcagtact	gatttggaaat	tcagtgtcaa	aagttagcaga	480
ggcttctctg	acccccaagg	ggtgacatgt	ggagcagtga	cactttcagc	agagagggtc	540
agagtggaca	acagggatta	taagaagtac	acagtggagt	gtcaggaagg	cagtgcctgc	600
ccctctgccc	aggagagcct	acccatcgag	gtcgtggtgg	atgctattca	caagctcaag	660
tatgaaaact	acaccagcag	cttcttcatc	agagacatca	tcaaaccaga	cccacccaca	720
aacctgcagc	tgaagccatt	gaaaaattct	cggcacgtgg	aggtcagctg	ggaataacccc	780
gacacctgga	gcaccccaaca	ttcctacttc	tccctgacat	tttgcgtaca	ggcccaggc	840
aagaacaata	gagaaaagaa	agatagactc	tgcgtggaca	agacctcagc	caaggtcgtg	900
tgccacaagg	atgccaagat	ccgcgtgaa	gcccgagacc	gctactata	ttcatcctgg	960
agcactggg	catctgtgtc	ctgcagttag	gttccacccc	caggatgaat	cttgg	1015

<210> 32

<211> 329

<212> PRT

<213> Canis familiaris

<400> 32

Met	His	Pro	Gln	Gln	Leu	Val	Ile	Ser	Trp	Phe	Ser	Leu	Val	Leu	Leu
1					5				10					15	
Ala	Ser	Ser	Leu	Met	Thr	Ile	Trp	Glu	Leu	Glu	Lys	Asp	Val	Tyr	Val
						20			25					30	
Val	Glu	Leu	Asp	Trp	His	Pro	Asp	Ala	Pro	Gly	Glu	Met	Val	Val	Leu
						35			40					45	
Thr	Cys	His	Thr	Pro	Glu	Glu	Asp	Asp	Ile	Thr	Trp	Thr	Ser	Ala	Gln
						50			55					60	
Ser	Ser	Glu	Val	Leu	Gly	Ser	Gly	Lys	Thr	Leu	Thr	Ile	Gln	Val	Lys
						65			70					80	
Glu	Phe	Gly	Asp	Ala	Gly	Gln	Tyr	Thr	Cys	His	Lys	Gly	Gly	Lys	Val
						85			90					95	
Leu	Ser	Arg	Ser	Leu	Leu	Ile	His	Lys	Lys	Glu	Asp	Gly	Ile	Trp	
						100			105					110	
Ser	Thr	Asp	Ile	Leu	Lys	Glu	Gln	Lys	Glu	Ser	Lys	Asn	Lys	Ile	Phe
						115			120					125	
Leu	Lys	Cys	Glu	Ala	Lys	Asn	Tyr	Ser	Gly	Arg	Phe	Thr	Cys	Trp	Trp
						130			135					140	
Leu	Thr	Ala	Ile	Ser	Thr	Asp	Leu	Lys	Phe	Ser	Val	Lys	Ser	Ser	Arg
						145			150					160	
Gly	Phe	Ser	Asp	Pro	Gln	Gly	Val	Thr	Cys	Gly	Ala	Val	Thr	Leu	Ser
						165			170					175	
Ala	Glu	Arg	Val	Arg	Val	Asp	Asn	Arg	Asp	Tyr	Lys	Lys	Tyr	Thr	Val
						180			185					190	
Glu	Cys	Gln	Glu	Gly	Ser	Ala	Cys	Pro	Ser	Ala	Glu	Glu	Ser	Leu	Pro
						195			200					205	
Ile	Glu	Val	Val	Val	Asp	Ala	Ile	His	Lys	Leu	Lys	Tyr	Glu	Asn	Tyr
						210			215					220	
Thr	Ser	Ser	Phe	Phe	Ile	Arg	Asp	Ile	Ile	Lys	Pro	Asp	Pro	Pro	Thr
						225			230					235	
Asn	Leu	Gln	Leu	Lys	Pro	Leu	Lys	Asn	Ser	Arg	His	Val	Glu	Val	Ser

	245	250	255												
Trp	Glu	Tyr	Pro	Asp	Thr	Trp	Ser	Thr	Pro	His	Ser	Tyr	Phe	Ser	Leu
	260		265		270										
Thr	Phe	Cys	Val	Gln	Ala	Gln	Gly	Lys	Asn	Asn	Arg	Glu	Lys	Lys	Asp
	275		280		285										
Arg	Leu	Cys	Val	Asp	Lys	Thr	Ser	Ala	Lys	Val	Val	Cys	His	Lys	Asp
	290		295		300										
Ala	Lys	Ile	Arg	Val	Gln	Ala	Arg	Asp	Arg	Tyr	Tyr	Ser	Ser	Ser	Trp
	305		310		315										320
Ser	Asp	Trp	Ala	Ser	Val	Ser	Cys	Ser							
	325														

<210> 33

<211> 1005

<212> DNA

<213> Cercocebus torquatus

<400> 33

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ctcccctcat	ggccatatatgg	gaactgaaga	aagacgtta	tgttgtagaa	ttggactgg	120
acccggatgc	ccctggagaa	atgggtgtcc	tcacctgtga	caccctgtaa	gaagatggta	180
tcacctggac	cttggaccag	atgggtgagg	tcttaggctc	tggcaaaacc	ctgaccatcc	240
aagtcaaaga	gtttggagat	gctggccagt	acacctgtca	caaaggaggc	gaggcttga	300
gccattcact	cctgctgcct	cacaaaaagg	aagatggaat	ttggtccact	gatattttaa	360
aggaccagaa	agaacccaaa	aatgagacct	ttctaagatg	cgaggccaaa	aattattctg	420
gacgtatcac	ctgctggtgg	ctgtcgacaa	tcagtaactga	tctgacattc	agtatcataa	480
gcagcagagg	ctcttctaac	ccccaaagggg	tgacgtgtgg	agccgctaca	ctctctgcag	540
agagggtcag	aggggacaat	aaggagtatg	agtactcagt	ggagtgccag	gaggacagtg	600
cctgcccagc	cgctgaggag	aggctgccc	ttgaggatcat	ggtggatgcc	attcacaagc	660
tcaagtatga	aaactacacc	agcagcttct	tcatcaggga	catcatcaaa	cccgaccac	720
ccaagaactt	gcagctgaag	ccattaaaga	attctggca	ggtggaggtc	agctgggagt	780
accctgacac	ctggagact	ccacattcct	acttctccct	gacattctgc	attcaggtcc	840
agggcaagag	caagagagaa	aagaaagata	gaatcttcac	agacaagacc	tcagccacgg	900
tcatctgccc	caaaaatgcc	agcttagcg	tgcaggccca	ggaccgctac	tatagctcat	960
cttggAACGA	atggacatct	gtgccctgca	gttagttct	gatcc		1005

<210> 34

<211> 328

<212> PRT

<213> Cercocebus torquatus

<400> 34

Met	Cys	His	Gln	Gln	Leu	Val	Ile	Ser	Trp	Phe	Ser	Leu	Val	Phe	Leu
1					5				10			15			
Ala	Ser	Pro	Leu	Met	Ala	Ile	Trp	Glu	Leu	Lys	Lys	Asp	Val	Tyr	Val
									20	25		30			
Val	Glu	Leu	Asp	Trp	Tyr	Pro	Asp	Ala	Pro	Gly	Glu	Met	Val	Val	Leu
									35	40		45			
Thr	Cys	Asp	Thr	Pro	Glu	Glu	Asp	Gly	Ile	Thr	Trp	Thr	Leu	Asp	Gln
									50	55		60			
Ser	Gly	Glu	Val	Leu	Gly	Ser	Gly	Lys	Thr	Leu	Thr	Ile	Gln	Val	Lys
									65	70		75		80	
Glu	Phe	Gly	Asp	Ala	Gly	Gln	Tyr	Thr	Cys	His	Lys	Gly	Gly	Glu	Ala
									85	90		95			
Leu	Ser	His	Ser	Leu	Leu	Leu	Pro	His	Lys	Lys	Glu	Asp	Gly	Ile	Trp
									100	105		110			
Ser	Thr	Asp	Ile	Leu	Lys	Asp	Gln	Lys	Glu	Pro	Lys	Asn	Glu	Thr	Phe

115	120	125
Leu Arg Cys Glu Ala Lys Asn Tyr Ser Gly Arg Ile Thr Cys Trp Trp		
130	135	140
Leu Ser Thr Ile Ser Thr Asp Leu Thr Phe Ser Ile Ile Ser Ser Arg		
145	150	155
Gly Ser Ser Asn Pro Gln Gly Val Thr Cys Gly Ala Ala Thr Leu Ser		
165	170	175
Ala Glu Arg Val Arg Gly Asp Asn Lys Glu Tyr Glu Tyr Ser Val Glu		
180	185	190
Cys Gln Glu Asp Ser Ala Cys Pro Ala Ala Glu Glu Arg Leu Pro Ile		
195	200	205
Glu Val Met Val Asp Ala Ile His Lys Leu Lys Tyr Glu Asn Tyr Thr		
210	215	220
Ser Ser Phe Phe Ile Arg Asp Ile Ile Lys Pro Asp Pro Pro Lys Asn		
225	230	235
Leu Gln Leu Lys Pro Leu Lys Asn Ser Arg Gln Val Glu Val Ser Trp		
245	250	255
Glu Tyr Pro Asp Thr Trp Ser Thr Pro His Ser Tyr Phe Ser Leu Thr		
260	265	270
Phe Cys Ile Gln Val Gln Gly Lys Ser Lys Arg Glu Lys Lys Asp Arg		
275	280	285
Ile Phe Thr Asp Lys Thr Ser Ala Thr Val Ile Cys Arg Lys Asn Ala		
290	295	300
Ser Phe Ser Val Gln Ala Gln Asp Arg Tyr Tyr Ser Ser Ser Trp Asn		
305	310	315
Glu Trp Thr Ser Val Pro Cys Ser		
325		

<210> 35
<211> 984
<212> DNA
<213> Marmota monax

<400> 35	
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acacctggag aaaaggttgtt cctcacctgt gacactcctg aagaagacgg catcacctgg	180
acctcagagc agagcagtga ggtcttaggc tccggcaaaa ccctgaccat tctagtcaaa	240
gagtttgaag acgctggcca ctacacctgc cgccagaggag gtgaagttct gagccagatg	300
ctcctgctgc ttcacaaaaa tgaagatggg atttggtcca ctgatattct gaagaaaaaaa	360
gaacctgaaa ataagaacct tctaaccatgc gaggcaaaaga attactctgg acgttttacc	420
tgcgttgtggc tgacggcaat cagtaactgtat gtgaacttca gtgtcaagag ccacagaggc	480
tcctctgacc ctcaagggtt gacgtgtggaa gaagcaactc tctctgcaga gagggtcaaa	540
atagagcaga gggagttacaa gaagtactcg gtgcagtgc aggaggacaa tgcctgcccc	600
accgctgagg agaccctgcc catcacagtg gtgggtggacg cagttcacaa gctcaagtac	660
aaaaactaca tcagcagctt cttcatcaga gacatcatca aacctgaccc acccaagaac	720
ctaaagatga agccatccaa gactcctcag caggtggagg tcacctggga gtaccggac	780
agctggagca ccccgcaactc ctacttctcc ctgacattct ctgtgcaggt ccagggcaaa	840
aagaagaaaa ggagcaatac tctccacgtg gataagacct cagtcacagt gacctgcccag	900
aagggtgcca aggtcagcgt gcaagcccg gaccgatact acaactcatc gtggagtgaa	960
tggcaacta tgtcctgccc ttag	984

<210> 36
<211> 327
<212> PRT
<213> Marmota monax

<400> 36

Met Cys Leu Gln Gln Leu Val Ile Ser Trp Val Ser Leu Val Trp Leu
1 5 10 15
Ala Ser Pro Leu Leu Ala Ile Trp Glu Leu Glu Lys Asn Val Tyr Val
20 25 30
Val Glu Leu Asp Trp His Pro Asp Thr Pro Gly Glu Lys Val Val Leu
35 40 45
Thr Cys Asp Thr Pro Glu Glu Asp Gly Ile Thr Trp Thr Ser Glu Gln
50 55 60
Ser Ser Glu Val Leu Gly Ser Gly Lys Thr Leu Thr Ile Leu Val Lys
65 70 75 80
Glu Phe Glu Asp Ala Gly His Tyr Thr Cys Arg Arg Gly Gly Glu Val
85 90 95
Leu Ser Gln Met Leu Leu Leu His Lys Asn Glu Asp Gly Ile Trp
100 105 110
Ser Thr Asp Ile Leu Lys Lys Glu Pro Glu Asn Lys Asn Leu Val
115 120 125
Thr Cys Glu Ala Lys Asn Tyr Ser Gly Arg Phe Thr Cys Trp Trp Leu
130 135 140
Thr Ala Ile Ser Thr Asp Val Asn Phe Ser Val Lys Ser His Arg Gly
145 150 155 160
Ser Ser Asp Pro Gln Gly Val Thr Cys Gly Glu Ala Thr Leu Ser Ala
165 170 175
Glu Arg Val Lys Ile Glu Gln Arg Glu Tyr Lys Lys Tyr Ser Val Gln
180 185 190
Cys Gln Glu Asp Asn Ala Cys Pro Thr Ala Glu Glu Thr Leu Pro Ile
195 200 205
Thr Val Val Val Asp Ala Val His Lys Leu Lys Tyr Glu Asn Tyr Ile
210 215 220
Ser Ser Phe Phe Ile Arg Asp Ile Ile Lys Pro Asp Pro Pro Lys Asn
225 230 235 240
Leu Lys Met Lys Pro Ser Lys Thr Pro Gln Gln Val Glu Val Thr Trp
245 250 255
Glu Tyr Pro Asp Ser Trp Ser Thr Pro His Ser Tyr Phe Ser Leu Thr
260 265 270
Phe Ser Val Gln Val Gln Gly Lys Lys Lys Arg Ser Asn Thr Leu
275 280 285
His Val Asp Lys Thr Ser Val Thr Val Thr Cys Gln Lys Gly Ala Lys
290 295 300
Val Ser Val Gln Ala Arg Asp Arg Tyr Tyr Asn Ser Ser Trp Ser Glu
305 310 315 320
Trp Ala Thr Met Ser Cys Pro
325